SEQUENCE LISTING

<110> Gish, Kurt
Mack, David

<120> Novel Methods of Diagnosing Breast Cancer, Compositions, and Methods of Screening for Breast Cancer Modulators

<130> A-69028/DJB/JJD

<140> US 09/747,371
<141> 2000-12-21

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<151> 2000-03-15

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<170> PatentIn version 3.0

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                       Met Gly Val Ala Gly Arg Asn Arg Pro Gly Ala
                       1               5                   10

gcc tgg gcg gtg ctg ctg ctg ctg ctg ctg ctg ccg cca ctg ctg ctg      161
Ala Trp Ala Val Leu Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
            15                  20                  25

ctg gcg ggg gcc gtc ccg ccg ggt cgg ggc cgt gcc gcg ggg ccg cag      209
Leu Ala Gly Ala Val Pro Pro Gly Arg Gly Arg Ala Ala Gly Pro Gln
        30                  35                  40

gag gat gta gat gag tgt gcc caa ggg cta gat gac tgc cat gcc gac      257
Glu Asp Val Asp Glu Cys Ala Gln Gly Leu Asp Asp Cys His Ala Asp
    45                  50                  55

gcc ctg tgt cag aac aca ccc acc tcc tac aag tgc tcc tgc aag cct      305
Ala Leu Cys Gln Asn Thr Pro Thr Ser Tyr Lys Cys Ser Cys Lys Pro
60                  65                  70                  75

ggc tac caa ggg gaa ggc agg cag tgt gag gac atc gat gaa tgt gga      353
Gly Tyr Gln Gly Glu Gly Arg Gln Cys Glu Asp Ile Asp Glu Cys Gly
                80                  85                  90

aat gag ctc aat gga ggc tgt gtc cat gac tgt ttg aat att cca ggc      401
Asn Glu Leu Asn Gly Gly Cys Val His Asp Cys Leu Asn Ile Pro Gly
            95                  100                 105

aat tat cgt tgc act tgt ttt gat ggc ttc atg ttg gct cat gac ggt      449
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Asn Tyr Arg Cys Thr Cys Phe Asp Gly Phe Met Leu Ala His Asp Gly
        110                 115                 120

cat aat tgt ctt gat gtg gac gag tgc ctg gag aac aat ggc ggc tgc      497
His Asn Cys Leu Asp Val Asp Glu Cys Leu Glu Asn Asn Gly Gly Cys
    125                 130                 135

cag cat acc tgt gtc aac gtc atg ggg agc tat gag tgc tgc tgc aag      545
Gln His Thr Cys Val Asn Val Met Gly Ser Tyr Glu Cys Cys Cys Lys
140                 145                 150                 155

gag ggg ttt ttc ctg agt gac aat cag cac acc tgc att cac cgc tcg      593
Glu Gly Phe Phe Leu Ser Asp Asn Gln His Thr Cys Ile His Arg Ser
                160                 165                 170

gaa gag ggc ctg agc tgc atg aat aag gat cac ggc tgt agt cac atc      641
Glu Glu Gly Leu Ser Cys Met Asn Lys Asp His Gly Cys Ser His Ile
            175                 180                 185

tgc aag gag gcc cca agg ggc agc gtc gcc tgt gag tgc agg cct ggt      689
Cys Lys Glu Ala Pro Arg Gly Ser Val Ala Cys Glu Cys Arg Pro Gly
        190                 195                 200

ttt gag ctg gcc aag aac cag aga gac tgc atc ttg acc tgt aac cat      737
Phe Glu Leu Ala Lys Asn Gln Arg Asp Cys Ile Leu Thr Cys Asn His
    205                 210                 215

ggg aac ggt ggg tgc cag cac tcc tgt gac gat aca gcc gat ggc cca      785
Gly Asn Gly Gly Cys Gln His Ser Cys Asp Asp Thr Ala Asp Gly Pro
220                 225                 230                 235

gag tgc agc tgc cat cca cag tac aag atg cac aca gat ggg agg agc      833
Glu Cys Ser Cys His Pro Gln Tyr Lys Met His Thr Asp Gly Arg Ser
                240                 245                 250

tgc ctt gag cga gag gac act gtc ctg gag gtg aca gag agc aac acc      881
Cys Leu Glu Arg Glu Asp Thr Val Leu Glu Val Thr Glu Ser Asn Thr
            255                 260                 265

aca tca gtg gtg gat ggg gat aaa cgg gtg aaa cgg cgg ctg ctc atg      929
Thr Ser Val Val Asp Gly Asp Lys Arg Val Lys Arg Arg Leu Leu Met
        270                 275                 280

gaa acg tgt gct gtc aac aat gga ggc tgt gac cgc acc tgt aag gat      977
Glu Thr Cys Ala Val Asn Asn Gly Gly Cys Asp Arg Thr Cys Lys Asp
    285                 290                 295

act tcg aca ggt gtc cac tgc agt tgt cct gtt gga ttc act ctc cag     1025
Thr Ser Thr Gly Val His Cys Ser Cys Pro Val Gly Phe Thr Leu Gln
300                 305                 310                 315

ttg gat ggg aag aca tgt aaa gat att gat gag tgc cag acc cgc aat     1073
Leu Asp Gly Lys Thr Cys Lys Asp Ile Asp Glu Cys Gln Thr Arg Asn
                320                 325                 330

gga ggt tgt gat cat ttc tgc aaa aac atc gtg ggc agt ttt gac tgc     1121
Gly Gly Cys Asp His Phe Cys Lys Asn Ile Val Gly Ser Phe Asp Cys
            335                 340                 345

ggc tgc aag aaa gga ttt aaa tta tta aca gat gag aag tct tgc caa     1169
Gly Cys Lys Lys Gly Phe Lys Leu Leu Thr Asp Glu Lys Ser Cys Gln
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          350                 355                 360

gat gtg gat gag tgc tct ttg gat agg acc tgt gac cac agc tgc atc      1217
Asp Val Asp Glu Cys Ser Leu Asp Arg Thr Cys Asp His Ser Cys Ile
    365                 370                 375

aac cac cct ggc aca ttt gct tgt gct tgc aac cga ggg tac acc ctg      1265
Asn His Pro Gly Thr Phe Ala Cys Ala Cys Asn Arg Gly Tyr Thr Leu
380                 385                 390                 395

tat ggc ttc acc cac tgt gga gac acc aat gag tgc agc atc aac aac      1313
Tyr Gly Phe Thr His Cys Gly Asp Thr Asn Glu Cys Ser Ile Asn Asn
                400                 405                 410

gga ggc tgt cag cag gtc tgt gtg aac aca gtg ggc agc tat gaa tgc      1361
Gly Gly Cys Gln Gln Val Cys Val Asn Thr Val Gly Ser Tyr Glu Cys
            415                 420                 425

cag tgc cac cct ggg tac aag ctc cac tgg aat aaa aaa gac tgt gtg      1409
Gln Cys His Pro Gly Tyr Lys Leu His Trp Asn Lys Lys Asp Cys Val
        430                 435                 440

gaa gtg aag ggg ctc ctg ccc aca agt gtg tca ccc cgt gtg tcc ctg      1457
Glu Val Lys Gly Leu Leu Pro Thr Ser Val Ser Pro Arg Val Ser Leu
    445                 450                 455

cac tgc ggt aag agt ggt gga gga gac ggg tgc ttc ctc aga tgt cac      1505
His Cys Gly Lys Ser Gly Gly Gly Asp Gly Cys Phe Leu Arg Cys His
460                 465                 470                 475

tct ggc att cac ctc tct tca gat gtc acc acc atc agg aca agt gta      1553
Ser Gly Ile His Leu Ser Ser Asp Val Thr Thr Ile Arg Thr Ser Val
                480                 485                 490

acc ttt aag cta aat gaa ggc aag tgt agt ttg aaa aat gct gag ctg      1601
Thr Phe Lys Leu Asn Glu Gly Lys Cys Ser Leu Lys Asn Ala Glu Leu
            495                 500                 505

ttt ccc gag ggt ctg cga cca gca cta cca gag aag cac agc tca gta      1649
Phe Pro Glu Gly Leu Arg Pro Ala Leu Pro Glu Lys His Ser Ser Val
        510                 515                 520

aaa gag agc ttc cgc tac gta aac ctt aca tgc agc tct ggc aag caa      1697
Lys Glu Ser Phe Arg Tyr Val Asn Leu Thr Cys Ser Ser Gly Lys Gln
    525                 530                 535

gtc cca gga gcc cct ggc cga cca agc acc cct aag gaa atg ttt atc      1745
Val Pro Gly Ala Pro Gly Arg Pro Ser Thr Pro Lys Glu Met Phe Ile
540                 545                 550                 555

act gtt gag ttt gag ctt gaa act aac caa aag gag gtg aca gct tct      1793
Thr Val Glu Phe Glu Leu Glu Thr Asn Gln Lys Glu Val Thr Ala Ser
                560                 565                 570

tgt gac ctg agc tgc atc gta aag cga acc gag aag cgg ctc cgt aaa      1841
Cys Asp Leu Ser Cys Ile Val Lys Arg Thr Glu Lys Arg Leu Arg Lys
            575                 580                 585

gcc atc cgc acg ctc aga aag gcc gtc cac agg gag cag ttt cac ctc      1889
Ala Ile Arg Thr Leu Arg Lys Ala Val His Arg Glu Gln Phe His Leu
        590                 595                 600
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cag ctc tca ggc atg aac ctc gac gtg gct aaa aag cct ccc aga aca      1937
Gln Leu Ser Gly Met Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr
    605                 610                 615

tct gaa cgc cag gca gag tcc tgt gga gtg ggc cag ggt cat gca gaa      1985
Ser Glu Arg Gln Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu
620                 625                 630                 635

aac caa tgt gtc agt tgc agg gct ggg acc tat tat gat gga gca cga      2033
Asn Gln Cys Val Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg
                640                 645                 650

gaa cgc tgc att tta tgt cca aat gga acc ttc caa aat gag gaa gga      2081
Glu Arg Cys Ile Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly
            655                 660                 665

caa atg act tgt gaa cca tgc cca aga cca gga aat tct ggg gcc ctg      2129
Gln Met Thr Cys Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu
        670                 675                 680

aag acc cca gaa gct tgg aat atg tct gaa tgt gga ggt ctg tgt caa      2177
Lys Thr Pro Glu Ala Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln
    685                 690                 695

cct ggt gaa tat tct gca gat ggc ttt gca cct tgc cag ctc tgt gcc      2225
Pro Gly Glu Tyr Ser Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala
700                 705                 710                 715

ctg ggc acg ttc cag cct gaa gct ggt cga act tcc tgc ttc ccc tgt      2273
Leu Gly Thr Phe Gln Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys
                720                 725                 730

gga gga ggc ctt gcc acc aaa cat cag gga gct act tcc ttt cag gac      2321
Gly Gly Gly Leu Ala Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp
            735                 740                 745

tgt gaa acc aga gtt caa tgt tca cct gga cat ttc tac aac acc acc      2369
Cys Glu Thr Arg Val Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr
        750                 755                 760

act cac cga tgt att cgt tgc cca gtg gga aca tac cag cct gaa ttt      2417
Thr His Arg Cys Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe
    765                 770                 775

gga aaa aat aat tgt gtt tct tgc cca gga aat act acg act gac ttt      2465
Gly Lys Asn Asn Cys Val Ser Cys Pro Gly Asn Thr Thr Thr Asp Phe
780                 785                 790                 795

gat ggc tcc aca aac ata acc cag tgt aaa aac aga aga tgt gga ggg      2513
Asp Gly Ser Thr Asn Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly
                800                 805                 810

gag ctg gga gat ttc act ggg tac att gaa tcc cca aac tac cca ggc      2561
Glu Leu Gly Asp Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly
            815                 820                 825

aat tac cca gcc aac acc gag tgt acg tgg acc atc aac cca ccc ccc      2609
Asn Tyr Pro Ala Asn Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro
        830                 835                 840
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aag cgc cgc atc ctg atc gtg gtc cct gag atc ttc ctg ccc ata gag      2657
Lys Arg Arg Ile Leu Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu
    845                 850                 855

gac gac tgt ggg gac tat ctg gtg atg cgg aaa acc tct tca tcc aat      2705
Asp Asp Cys Gly Asp Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn
860                 865                 870                 875

tct gtg aca aca tat gaa acc tgc cag acc tac gaa cgc ccc atc gcc      2753
Ser Val Thr Thr Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala
                880                 885                 890

ttc acc tcc agg tca aag aag ctg tgg att cag ttc aag tcc aat gaa      2801
Phe Thr Ser Arg Ser Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu
            895                 900                 905

ggg aac agc gct aga ggg ttc cag gtc cca tac gtg aca tat gat gag      2849
Gly Asn Ser Ala Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu
        910                 915                 920

gac tac cag gaa ctc att gaa gac ata gtt cga gat ggc agg ctc tat      2897
Asp Tyr Gln Glu Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr
    925                 930                 935

gca tct gag aac cat cag gaa ata ctt aag gat aag aaa ctt atc aag      2945
Ala Ser Glu Asn His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys
940                 945                 950                 955

gct ctg ttt gat gtc ctg gcc cat ccc cag aac tat ttc aag tac aca      2993
Ala Leu Phe Asp Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr
                960                 965                 970

gcc cag gag tcc cga gag atg ttt cca aga tcg ttc atc cga ttg cta      3041
Ala Gln Glu Ser Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu
            975                 980                 985

cgt tcc aaa gtg tcc agg ttt ttg aga cct tac aaa tga ctcagcccac       3090
Arg Ser Lys Val Ser Arg Phe Leu Arg Pro Tyr Lys
        990                 995

gtgccactca atacaaatgt tctgctatag ggttggtggg acagagctgt cttccttctg    3150

catgtcagca cagtcgggta ttgctgcctc ccgtatcagt gactcattag agttcaattt    3210

ttatagataa tacagatatt ttggtaaatt gaacttggtt tttctttccc agcatcgtgg    3270

atgtagactg agaatggctt tgagtggcat cagcttctca ctgctgtggg cggatgtctt    3330

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gcttattctg aaacttcagc ttcctctagc ccggccctct ctaagggagc cctctgcact    3510

cgtgtgcagg ctctgaccag gcagaacagg caagagggga gggaaggaga cccctgcagg    3570

ctccctccac ccaccttgag acctgggagg actcagtttc tccacagcct tctccagcct    3630

gtgtgataca agtttgatcc caggaacttg agttctaagc agtgctcgtg aaaaaaaaaa    3690

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            20                  25                  30

Pro Pro Gly Arg Gly Arg Ala Ala Gly Pro Gln Glu Asp Val Asp Glu
        35                  40                  45

Cys Ala Gln Gly Leu Asp Asp Cys His Ala Asp Ala Leu Cys Gln Asn
    50                  55                  60

Thr Pro Thr Ser Tyr Lys Cys Ser Cys Lys Pro Gly Tyr Gln Gly Glu
65                  70                  75                  80

Gly Arg Gln Cys Glu Asp Ile Asp Glu Cys Gly Asn Glu Leu Asn Gly
                85                  90                  95

Gly Cys Val His Asp Cys Leu Asn Ile Pro Gly Asn Tyr Arg Cys Thr
            100                 105                 110

Cys Phe Asp Gly Phe Met Leu Ala His Asp Gly His Asn Cys Leu Asp
        115                 120                 125

Val Asp Glu Cys Leu Glu Asn Asn Gly Gly Cys Gln His Thr Cys Val
    130                 135                 140

Asn Val Met Gly Ser Tyr Glu Cys Cys Cys Lys Glu Gly Phe Phe Leu
145                 150                 155                 160

Ser Asp Asn Gln His Thr Cys Ile His Arg Ser Glu Glu Gly Leu Ser
                165                 170                 175

Cys Met Asn Lys Asp His Gly Cys Ser His Ile Cys Lys Glu Ala Pro
            180                 185                 190

Arg Gly Ser Val Ala Cys Glu Cys Arg Pro Gly Phe Glu Leu Ala Lys
        195                 200                 205
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Asn Gln Arg Asp Cys Ile Leu Thr Cys Asn His Gly Asn Gly Gly Cys
210 215 220

Gln His Ser Cys Asp Asp Thr Ala Asp Gly Pro Glu Cys Ser Cys His
225 230 235 240

Pro Gln Tyr Lys Met His Thr Asp Gly Arg Ser Cys Leu Glu Arg Glu
245 250 255

Asp Thr Val Leu Glu Val Thr Glu Ser Asn Thr Thr Ser Val Val Asp
260 265 270

Gly Asp Lys Arg Val Lys Arg Arg Leu Leu Met Glu Thr Cys Ala Val
275 280 285

Asn Asn Gly Gly Cys Asp Arg Thr Cys Lys Asp Thr Ser Thr Gly Val
290 295 300

His Cys Ser Cys Pro Val Gly Phe Thr Leu Gln Leu Asp Gly Lys Thr
305 310 315 320

Cys Lys Asp Ile Asp Glu Cys Gln Thr Arg Asn Gly Gly Cys Asp His
325 330 335

Phe Cys Lys Asn Ile Val Gly Ser Phe Asp Cys Gly Cys Lys Lys Gly
340 345 350

Phe Lys Leu Leu Thr Asp Glu Lys Ser Cys Gln Asp Val Asp Glu Cys
355 360 365

Ser Leu Asp Arg Thr Cys Asp His Ser Cys Ile Asn His Pro Gly Thr
370 375 380

Phe Ala Cys Ala Cys Asn Arg Gly Tyr Thr Leu Tyr Gly Phe Thr His
385 390 395 400

Cys Gly Asp Thr Asn Glu Cys Ser Ile Asn Asn Gly Gly Cys Gln Gln
405 410 415

Val Cys Val Asn Thr Val Gly Ser Tyr Glu Cys Gln Cys His Pro Gly
420 425 430

Tyr Lys Leu His Trp Asn Lys Lys Asp Cys Val Glu Val Lys Gly Leu
435 440 445

Leu Pro Thr Ser Val Ser Pro Arg Val Ser Leu His Cys Gly Lys Ser

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     450                 455                 460

Gly Gly Gly Asp Gly Cys Phe Leu Arg Cys His Ser Gly Ile His Leu
465                 470                 475                 480

Ser Ser Asp Val Thr Thr Ile Arg Thr Ser Val Thr Phe Lys Leu Asn
                485                 490                 495

Glu Gly Lys Cys Ser Leu Lys Asn Ala Glu Leu Phe Pro Glu Gly Leu
            500                 505                 510

Arg Pro Ala Leu Pro Glu Lys His Ser Ser Val Lys Glu Ser Phe Arg
        515                 520                 525

Tyr Val Asn Leu Thr Cys Ser Ser Gly Lys Gln Val Pro Gly Ala Pro
    530                 535                 540

Gly Arg Pro Ser Thr Pro Lys Glu Met Phe Ile Thr Val Glu Phe Glu
545                 550                 555                 560

Leu Glu Thr Asn Gln Lys Glu Val Thr Ala Ser Cys Asp Leu Ser Cys
                565                 570                 575

Ile Val Lys Arg Thr Glu Lys Arg Leu Arg Lys Ala Ile Arg Thr Leu
            580                 585                 590

Arg Lys Ala Val His Arg Glu Gln Phe His Leu Gln Leu Ser Gly Met
        595                 600                 605

Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr Ser Glu Arg Gln Ala
    610                 615                 620

Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val Ser
625                 630                 635                 640

Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile Leu
                645                 650                 655

Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys Glu
            660                 665                 670

Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu Ala
        675                 680                 685

Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Gly Glu Tyr Ser
    690                 695                 700
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Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Thr Phe Gln
705 710 715 720

Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Gly Leu Ala
725 730 735

Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg Val
740 745 750

Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys Ile
755 760 765

Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn Cys
770 775 780

Val Ser Cys Pro Gly Asn Thr Thr Thr Asp Phe Asp Gly Ser Thr Asn
785 790 795 800

Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp Phe
805 810 815

Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala Asn
820 825 830

Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile Leu
835 840 845

Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly Asp
850 855 860

Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr Tyr
865 870 875 880

Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg Ser
885 890 895

Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala Arg
900 905 910

Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu Leu
915 920 925

Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His
930 935 940

Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp Val
945   950   955   960

Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser Arg
                965   970   975

Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val Ser
            980   985   990

Arg Phe Leu Arg Pro Tyr Lys
        995

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1   5   10   15

Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Ala Ala Ala Val Pro Pro
            20   25   30

Asp Arg Gly Leu Thr Asn Gly Pro Ser Glu Asp Val Asp Glu Cys Ala
        35   40   45

Gln Gly Leu Asp Asp Cys His Ala Asp Ala Leu Cys Gln Asn Thr Pro
    50   55   60

Thr Ser Tyr Lys Cys Ser Cys Lys Pro Gly Tyr Gln Gly Glu Gly Arg
65   70   75   80

Gln Cys Glu Asp Met Asp Glu Cys Asp Asn Thr Leu Asn Gly Gly Cys
                85   90   95

Val His Asp Cys Leu Asn Ile Pro Gly Asn Tyr Arg Cys Thr Cys Phe
            100   105   110

Asp Gly Phe Met Leu Ala His Asp Gly His Asn Cys Leu Asp Met Asp
        115   120   125

Glu Cys Leu Glu Asn Asn Gly Gly Cys Gln His Ile Cys Thr Asn Val
    130   135   140

Ile Gly Ser Tyr Glu Cys Arg Cys Lys Glu Gly Phe Phe Leu Ser Asp
145   150   155   160

Asn Gln His Thr Cys Ile His Arg Ser Glu Glu Gly Leu Ser Cys Met
                165   170   175

Asn Lys Asp His Gly Cys Gly His Ile Cys Lys Glu Ala Pro Arg Gly
            180   185   190

Ser Val Ala Cys Glu Cys Arg Pro Gly Phe Glu Leu Ala Lys Asn Gln

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        195                 200                 205

Lys Asp Cys Ile Leu Thr Cys Asn His Gly Asn Gly Gly Cys Gln His
    210                 215                 220

Ser Cys Glu Asp Thr Ala Glu Gly Pro Glu Cys Ser Cys His Pro Arg
225                 230                 235                 240

Tyr Arg Leu His Ala Asp Gly Arg Ser Cys Leu Glu Gln Glu Gly Thr
                245                 250                 255

Val Leu Glu Gly Thr Glu Ser Asn Ala Thr Ser Val Ala Asp Gly Asp
            260                 265                 270

Lys Arg Val Lys Arg Arg Leu Leu Met Glu Thr Cys Ala Val Asn Asn
        275                 280                 285

Gly Gly Cys Asp Arg Thr Cys Lys Asp Thr Ser Thr Gly Val His Cys
    290                 295                 300

Ser Cys Pro Thr Gly Phe Thr Leu Gln Val Asp Gly Lys Thr Cys Lys
305                 310                 315                 320

Asp Ile Asp Glu Cys Gln Thr Arg Asn Gly Gly Cys Asn His Phe Cys
                325                 330                 335

Lys Asn Thr Val Gly Ser Phe Asp Cys Ser Cys Lys Lys Gly Phe Lys
            340                 345                 350

Leu Leu Thr Asp Glu Lys Ser Cys Gln Asp Val Asp Glu Cys Ser Leu
        355                 360                 365

Glu Arg Thr Cys Asp His Ser Cys Ile Asn His Pro Gly Thr Phe Ile
    370                 375                 380

Cys Ala Cys Asn Pro Gly Tyr Thr Leu Tyr Ser Phe Thr His Cys Gly
385                 390                 395                 400

Asp Thr Asn Glu Cys Ser Val Asn Asn Gly Gly Cys Gln Gln Val Cys
                405                 410                 415

Ile Asn Thr Val Gly Ser Tyr Glu Cys Gln Cys His Pro Gly Phe Lys
            420                 425                 430

Leu His Trp Asn Lys Lys Asp Cys Val Glu Val Lys Gly Phe Pro Pro
        435                 440                 445

Thr Ser Met Thr Pro Arg Val Ser Leu His Cys Gly Lys Ser Gly Gly
    450                 455                 460

Gly Asp Arg Cys Phe Leu Arg Cys Arg Ser Gly Ile His Leu Ser Ser
465                 470                 475                 480

Asp Val Val Thr Val Arg Thr Ser Val Thr Phe Lys Leu Asn Glu Gly
                485                 490                 495

Lys Cys Ser Leu Gln Lys Ala Lys Leu Ser Pro Glu Gly Leu Arg Pro
            500                 505                 510

Ala Leu Pro Glu Arg His Ser Ser Val Lys Glu Ser Phe Gln Tyr Ala
        515                 520                 525
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Asn Leu Thr Cys Ser Pro Gly Lys Gln Val Pro Gly Ala Leu Gly Arg
530 535 540

Leu Asn Ala Pro Lys Glu Met Phe Ile Thr Val Glu Phe Glu Arg Glu
545 550 555 560

Thr Tyr Glu Lys Glu Val Thr Ala Ser Cys Asn Leu Ser Cys Val Val
565 570 575

Lys Arg Thr Glu Lys Arg Leu Arg Lys Ala Leu Arg Thr Leu Lys Arg
580 585 590

Ala Ala His Arg Glu Gln Phe His Leu Gln Leu Ser Gly Met Asp Leu
595 600 605

Asp Met Ala Lys Thr Pro Ser Arg Val Ser Gly Gln His Glu Glu Thr
610 615 620

Cys Gly Val Gly Gln Gly His Glu Glu Ser Gln Cys Val Ser Cys Arg
625 630 635 640

Ala Gly Thr Tyr Tyr Asp Gly Ser Gln Glu Arg Cys Ile Leu Cys Pro
645 650 655

Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Val Thr Cys Glu Pro Cys
660 665 670

Pro Arg Pro Glu Asn Leu Gly Ser Leu Lys Ile Ser Glu Ala Trp Asn
675 680 685

Val Ser Asp Cys Gly Gly Leu Cys Gln Pro Gly Glu Tyr Ser Ala Asn
690 695 700

Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Thr Phe Gln Pro Asp
705 710 715 720

Val Gly Arg Thr Ser Cys Leu Ser Cys Gly Gly Gly Leu Pro Thr Lys
725 730 735

His Leu Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg Val Gln Cys
740 745 750

Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys Ile Arg Cys
755 760 765

Pro Leu Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn Cys Val Ser
770 775 780

Cys Pro Gly Asn Thr Thr Thr Asp Phe Asp Gly Ser Thr Asn Ile Thr
785 790 795 800

Gln Cys Lys Asn Arg Lys Cys Gly Gly Glu Leu Gly Asp Phe Thr Gly
805 810 815

Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala Asn Ser Glu
820 825 830

Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile Leu Ile Val
835 840 845

```
Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly Asp Tyr Leu
    850                 855                 860

Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr Tyr Glu Thr
865                 870                 875                 880

Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg Ser Lys Lys
                885                 890                 895

Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala Arg Gly Phe
            900                 905                 910

Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu Leu Ile Glu
        915                 920                 925

Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu
    930                 935                 940

Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp Val Leu Ala
945                 950                 955                 960

His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser Arg Glu Met
                965                 970                 975

Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val Ser Arg Phe
            980                 985                 990

Leu Arg Pro Tyr Lys
        995
```

<210> 4
<211> 5
<212> PRT
<213> Unknown

<220>
<223> Cytokine receptor exctacelluar motif found in many species.

<220>
<221> UNSURE
<222> (3)..(3)
<223> "Xaa" at position 3 can be any amino acid.

<400> 4

```
Trp Ser Xaa Trp Ser
1               5
```